

For the reasons explained above and pending reconsideration by the Examiner of the restriction requirement, Applicants have not canceled non-elected claims 57-74 from Group IV.

Kindly amend the above-referenced patent application as follows.

In the claims:

Cancel non-elected claims 4-56 and 75-144 and add new claims 145-156 as follows.

145. (New) The method of claim 1, wherein said sequence-specific binding activity of said step (a) comprises a sequence-specific cleavage agent and said bound subset retained by said sequence-specific binding activity is cleaved by said cleavage agent to produce nucleic acid fragments, and wherein said fragments are operatively linked with a separation element to separate said linked fragments.

146. (New) The method of claim 1, wherein said nucleic acid sample is from one or more individuals and said conditions which permit sequence-specific binding in said contacting step (a) also permit fragmenting of said nucleic acid sample to an average fragment length to produce a subset of nucleic acid fragments.

147. (New) The method of claim 146, wherein said molecule comprising said sequence-specific binding activity also comprises sequence-specific cleavage, and said subset of nucleic acid fragments is separated based on the presence or absence of a nucleotide sequence within said fragments.

148. (New) The method of claim 1, wherein said nucleic acid sample is from one or more individuals and said contacting step (a) comprises contacting said nucleic acid sample with said molecule to produce said subset of nucleic acid molecules which is enriched for molecules comprising the sequence recognized by the sequence specific binding activity, wherein said subset is fragmented and bound based upon fragment size.

149. (New) The method of claim 145, 146 or 148, wherein said nucleic acid sample comprises nucleic acid from one or more individuals and said method further comprising the step of identifying a nucleic acid sequence polymorphism in said one or more individuals.

150. (New) The method of claim 1, wherein said detecting comprises DNA sequencing.

151. (New) The method of claim 1, wherein said detecting comprises denaturing HPLC.

152. (New) The method of claim 1, wherein said detecting comprises electrophoresis.

153. (New) The method of claim 1, wherein said detecting comprises formation of duplex DNA and detection of a nucleic acid duplex mismatch.

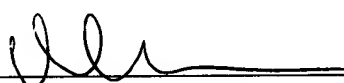
154. (New) The method of claim 2, wherein said restriction endonuclease DNA recognition domain comprises a restriction endonuclease.

155. (New) The method of claim 154, wherein said restriction endonuclease cleaves DNA infrequently.

156. (New) The method of claim 155 wherein the infrequently cleaving restriction endonuclease is selected from the group consisting of *AscI*, *BssHII*, *EagI*, *NheI*, *NotI*, *PacI*, *PmeI*, *RsrII*, *Sall*, *SbfI*, *SfiI*, *SgrAI*, *SpeI*, *SrfI*, and *SwaI* restriction endonucleases.

Respectfully submitted,

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